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1633

TECH CENTER 1600/2900

444

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/771,045A

DATE: 05/03/2001
TIME: 12:58:01

Input Set : A:\1134CSEQLIST.TXT
Output Set: N:\CRF3\05032001\I771045A.raw

ENTERED

4 <110> APPLICANT: Duvick, Jonathan P.
 5 Gilliam, Jacob T.
 6 Maddox, Joyce R.
 8 <120> TITLE OF INVENTION: Amino Polyol Amine Oxidase
 9 Polynucleotides and Related Polypeptides and Methods of Use
 12 <130> FILE REFERENCE: 1134C
 14 <140> CURRENT APPLICATION NUMBER: 09/771,045A
 15 <141> CURRENT FILING DATE: 2001-01-26
 17 <150> PRIOR APPLICATION NUMBER: US 60/092,936
 18 <151> PRIOR FILING DATE: 1998-07-15
 20 <150> PRIOR APPLICATION NUMBER: US 60/135,391
 21 <151> PRIOR FILING DATE: 1999-05-21
 23 <150> PRIOR APPLICATION NUMBER: US 09/352,159
 24 <151> PRIOR FILING DATE: 1999-07-12
 26 <150> PRIOR APPLICATION NUMBER: US 09/352,168
 27 <151> PRIOR FILING DATE: 1999-07-12
 29 <160> NUMBER OF SEQ ID NOS: 53
 31 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 33 <210> SEQ ID NO: 1
 34 <211> LENGTH: 372
 35 <212> TYPE: DNA
 36 <213> ORGANISM: Exophiala spinifera
 38 <220> FEATURE:
 39 <221> NAME/KEY: misc_feature
 40 <222> LOCATION: (346)...(346)
 41 <223> OTHER INFORMATION: n = A,T,C or G
 43 <400> SEQUENCE: 1
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 45 gcttggactg ttgggaccac ttccgtcccc ggtctccgac catgaaaacag gtaatggacc 120
 46 attgtcgatc gacgtcgatc ctggtatctc tgccaaatga gatggggtca cagctcgatt 180
 47 ggaggacgcc cgagaagctt tgttcgcgcc accacggctt gtcccatacg aagactatct 240
 48 tgctatagta gcccaggata gaattttccg ccaatgcttg cttctcgcc ggaagaggtg 300
 49 gtgaaaatgt caaggtggga tacaaggttt tcggtaacga aaccancacc tttttgcttc 360
 50 ggaacacggc gc 372
 52 <210> SEQ ID NO: 2
 53 <211> LENGTH: 182
 54 <212> TYPE: DNA
 55 <213> ORGANISM: Exophiala spinifera
 57 <400> SEQUENCE: 2
 58 gaattttccg ccaatgcttg cttctcgcc ggaagaggtg gtgaaaatgt caaggtggga 60
 59 tacaaggttt tcggtaacga aaccaccacc tttttgcttc ggaacacggc gcccggggcc 120
 60 gatcgacttg tacagccgga tgccgactgc tcaatttcag cgacgggggt gttgaggtgc 180
 61 ac 182
 63 <210> SEQ ID NO: 3
 64 <211> LENGTH: 29
 65 <212> TYPE: DNA
 66 <213> ORGANISM: Artificial Sequence

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68 <220> FEATURE:
69 <223> OTHER INFORMATION: Designed oligonucleotide for 3' RACE, N21965
72 <400> SEQUENCE: 3
73 tggtttcggtt accgacaacc ttgtatccc 29
75 <210> SEQ ID NO: 4
76 <211> LENGTH: 28
77 <212> TYPE: DNA
78 <213> ORGANISM: Artificial Sequence
80 <220> FEATURE:
81 <223> OTHER INFORMATION: Designed oligonucleotide for 5' RACE, 21968
83 <400> SEQUENCE: 4
84 gagttgggcc cagacagact tttgtcgt 28
86 <210> SEQ ID NO: 5
87 <211> LENGTH: 1389
88 <212> TYPE: DNA
89 <213> ORGANISM: Exophiala spinifera
91 <220> FEATURE:
92 <221> NAME/KEY: CDS
93 <222> LOCATION: (1)...(1386)
95 <400> SEQUENCE: 5
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97 Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly Leu
98 1 5 10 15
100 gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt 96
101 Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
102 20 25 30
104 gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt 144
105 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
106 35 40 45
108 ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac 192
109 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
110 50 55 60
112 agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag 240
113 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
114 65 70 75 80
116 ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac 288
117 Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
118 85 90 95
120 ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag 336
121 Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
122 100 105 110
124 gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc 384
125 Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
126 115 120 125
128 gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg 432
129 Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
130 130 135 140
132 ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg 480
133 Leu Asp Ser Val Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu

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134	145	150	155	160	
136	cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt				528
137	Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly				
138	165	170	175		
140	gtg gaa gcc cac gag atc agc atg ctt ttc ctc acc gac tac atc aag				576
141	Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys				
142	180	185	190		
144	agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg				624
145	Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly				
146	195	200	205		
148	cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg				672
149	Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met				
150	210	215	220		
152	tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct				720
153	Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala				
154	225	230	235	240	
156	gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc				768
157	Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly				
158	245	250	255		
160	gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg				816
161	Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu				
162	260	265	270		
164	tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca				864
165	Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala				
166	275	280	285		
168	ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta				912
169	Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val				
170	290	295	300		
172	tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa				960
173	Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln				
174	305	310	315	320	
176	tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc				1008
177	Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val				
178	325	330	335		
180	gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga ccg				1056
181	Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg				
182	340	345	350		
184	aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac				1104
185	Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp				
186	355	360	365		
188	caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg				1152
189	Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro				
190	370	375	380		
192	gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga				1200
193	Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly				
194	385	390	395	400	
196	gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg				1248
197	Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser				
198	405	410	415		

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200	gct	ctc	aga	acg	ccg	tcc	aag	agt	gtt	cat	ttc	gta	acg	gag	acg		1296		
201	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr			
202																420	425	430	
204	tct	tta	gtt	tgg	aaa	ggg	tat	atg	gaa	ggg	gcc	ata	cga	tcg	ggt	caa		1344	
205	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln			
206																435	440	445	
208	cga	ggc	gtc	gca	gaa	gtt	gtg	gtc	agc	ctg	gtc	cca	gca	gca				1386	
209	Arg	Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala					
210																450	455	460	
212	tag																	1389	
214	<210>	SEQ	ID	NO:	6														
215	<211>	LENGTH:	462																
216	<212>	TYPE:	PRT																
217	<213>	ORGANISM:	Exophiala spinifera																
219	<400>	SEQUENCE:	6																
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221	1						5						10				15		
222	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu			
223													20	25	30				
224	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly			
225													35	40	45				
226	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp			
227													50	55	60				
228	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu			
229													65	70	75	80			
230	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp			
231													85	90	95				
232	Gly	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu				
233													100	105	110				
234	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile			
235													115	120	125				
236	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg			
237													130	135	140				
238	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu			
239													145	150	155	160			
240	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Gly				
241													165	170	175				
242	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys			
243													180	185	190				
244	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly			
245													195	200	205				
246	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met			
247													210	215	220				
248	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala			
249													225	230	235	240			
250	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly			
251													245	250	255				
252	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu			
253													260	265	270				

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254 Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala
 255 275 280 285
 256 Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val
 257 290 295 300
 258 Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
 259 305 310 315 320
 260 Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
 261 325 330 335
 262 Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg
 263 340 345 350
 264 Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
 265 355 360 365
 266 Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
 267 370 375 380
 268 Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
 269 385 390 395 400
 270 Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
 271 405 410 415
 272 Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
 273 420 425 430
 274 Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
 275 435 440 445
 276 Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 277 450 455 460
 279 <210> SEQ ID NO: 7
 280 <211> LENGTH: 1442
 281 <212> TYPE: DNA
 282 <213> ORGANISM: Exophiala spinifera
 284 <220> FEATURE:
 285 <221> NAME/KEY: CDS
 286 <222> LOCATION: (1)...(646)
 288 <221> NAME/KEY: intron
 289 <222> LOCATION: (647)...(699)
 291 <221> NAME/KEY: CDS
 292 <222> LOCATION: (700)...(1439)
 294 <400> SEQUENCE: 7
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 296 Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly Leu
 297 1 5 10 15
 299 gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt 96
 300 Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
 301 20 25 30
 303 gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt 144
 304 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
 305 35 40 45
 307 ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac 192
 308 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
 309 50 55 60
 311 agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag 240

Please Note:

Use of n and/ r Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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L:49 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:352 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 7
L:1340 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:1341 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:3173 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:3174 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:4214 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:4275 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40